



## SEQUENCE LISTING

<110> Jalkanen, Markku  
Darwish, Kamel El  
Lindhahl, Ulf  
Li, Jin-Ping

<120> Glucuronyl C5-Epimerase, DNA Encoding the Same and Uses Thereof

<130> 1708.0280002

<140> US 10/005,647

<141> 2001-12-07

<150> US 60/304,180

<151> 2000-12-08

<150> US 09/732,026

<151> 2000-12-08

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 1854

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1854)

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1			5				10					15				
tgt	gcg	cta	ttc	act	ttg	gtc	aca	gta	ctt	ttg	tgg	aat	aag	tgt	tcc	96
Cys	Ala	Leu	Phe	Thr	Leu	Val	Thr	Val	Leu	Leu	Trp	Asn	Lys	Cys	Ser	
		20					25				30					
agc	gac	aaa	gca	atc	cag	ttt	cct	cgg	cac	ttg	agt	agt	gga	ttc	aga	144
Ser	Asp	Lys	Ala	Ile	Gln	Phe	Pro	Arg	His	Leu	Ser	Ser	Gly	Phe	Arg	
		35					40				45					
gtg	gat	gga	tta	gaa	aaa	aga	tca	gca	gca	tct	gaa	agt	aac	cac	tat	192
Val	Asp	Gly	Leu	Glu	Lys	Arg	Ser	Ala	Ala	Ser	Glu	Ser	Asn	His	Tyr	
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gcc	aac	cac	ata	gcc	aaa	cag	cag	tca	gaa	gag	gca	ttt	cct	cag	gaa	240
Ala	Asn	His	Ile	Ala	Lys	Gln	Gln	Ser	Glu	Glu	Ala	Phe	Pro	Gln	Glu	

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caa cag aag gca ccc cct gtt gtt ggg ggc ttc aat agc aac ggg gga				288
Gln Gln Lys Ala Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly	85	90	95	
agc aag gtg tta ggg ctc aaa tat gaa gag att gac tgt ctc ata aac				336
Ser Lys Val Leu Gly Leu Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn	100	105	110	
gat gag cac acc att aaa ggg aga cga gag ggg aat gaa gtt ttc ctt				384
Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu	115	120	125	
cca ttc act tgg gta gag aaa tac ttt gat gtt tat gga aaa gtg gtc				432
Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val	130	135	140	
cag tat gac ggc tat gat cga ttt gaa ttc tct cat agc tat tcc aaa				480
Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys	145	150	155	160
gtc tat gca cag aga tca cct tat cac cct gac ggt gtg ttt atg tcc				528
Val Tyr Ala Gln Arg Ser Pro Tyr His Pro Asp Gly Val Phe Met Ser	165	170	175	
ttt gaa ggc tac aat gtg gaa gtc cga gac aga gtc aaa tgt ata agt				576
Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser	180	185	190	
gga gtt gaa ggt gtg cca tta tct acc cag tgg ggg cct caa ggc tat				624
Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr	195	200	205	
ttc tac cca atc cag att gca cag tat ggg cta agt cat tac agc aag				672
Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys	210	215	220	
aat cta acc gag aaa ccc cct cac ata gaa gta tat gaa aca gca gaa				720
Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu	225	230	235	240
gac agg gac aga aac atc aga cct aat gaa tgg act gtg ccc aag ggg				768
Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly	245	250	255	
tgc ttc atg gcc agt gtg gca gac aag tct aga tcc acc aat gtt aaa				816
Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys	260	265	270	
cag ttt att gct cca gaa acc agt gaa ggt gtg tct ttg cag ctg gga				864
Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly	275	280	285	
aac aca aaa gac ttc att att tca ttt gac ctc aag ctt tta aca aat				912
Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn	290	295	300	
ggg agt gtg tct gtg gtt ctg gag acc aca gaa aag aat cag ctc ttc				960
Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe	305	310	315	320

act gtg cat tat gtc tca aac acc cag ctg att gct ttc aga gac agg	1008
Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg	
325 330 335	
gac ata tac tac ggc att ggg ccc aga act tca tgg agt aca gtt acc	1056
Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr	
340 345 350	
aga gac ctg gtc act gac ctc agg aaa gga gtg ggc ctt tct aac aca	1104
Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr	
355 360 365	
aaa gct gtc aag cca acc aaa atc atg ccc aaa aag gtg gtt agg ttg	1152
Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu	
370 375 380	
att gca aaa ggg aag gga ttc ctg gac aac att acc atc tca acc aca	1200
Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr	
385 390 395 400	
gcc cac atg gct gca ttc ttt gct gca agt gac tgg cta gtg agg aac	1248
Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn	
405 410 415	
cag gat gag aaa ggt ggc tgg cca att atg gtg acc cgg aag tta ggg	1296
Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly	
420 425 430	
gaa ggg ttt aaa tct tta gaa cca gga tgg tac tct gcc atg gca caa	1344
Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln	
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ggg caa gcc atc tct acc tta gtc agg gcc tat ctt cta acg aaa gac	1392
Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp	
450 455 460	
tat gta ttc ctc agt tca gct tta agg gca aca gcc cca tac aag ttt	1440
Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe	
465 470 475 480	
ccg tca gag cag cat gga gtt aaa gcc gtg ttc atg aat aaa cat gac	1488
Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp	
485 490 495	
tgg tat gaa gaa tat cca acc aca cct agc tct ttt gtt tta aat ggc	1536
Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly	
500 505 510	
ttt atg tat tct tta att ggg ctg tat gac cta aaa gaa aca gca ggg	1584
Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly	
515 520 525	
gag aca ctt ggg aaa gaa gca agg tcc ttg tac gag cgc ggc atg gaa	1632
Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu	
530 535 540	
tct ctt aaa gcc atg ctg ccc ttg tat gat act ggc tcc ggg acc atc	1680
Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile	
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tat gac ctc cgc cac ttc atg ctt ggc att gct ccc aac ctg gcc cgc	1728
Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg	
565 570 575	

tgg gac tat cac acc acc cac att aac cag ctg cag ctg ctc agc acc	1776
Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr	
580 585 590	

atc gat gag tcc cca atc ttc aaa gaa ttt gtc aag agg tgg aaa agc	1824
Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser	
595 600 605	

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<212> PRT

<213> Mus musculus

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Ser Asp Lys Ala Ile Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg
35 40 45

Val Asp Gly Leu Glu Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr
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Ala Asn His Ile Ala Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu
65 70 75 80

Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly
85 90 95

Ser Lys Val Leu Gly Leu Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn
100 105 110

Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu
115 120 125

Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val  
 130 135 140

Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys  
 145 150 155 160

Val Tyr Ala Gln Arg Ser Pro Tyr His Pro Asp Gly Val Phe Met Ser  
 165 170 175

Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser  
 180 185 190

Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr  
 195 200 205

Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys  
 210 215 220

Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu  
 225 230 235 240

Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly  
 245 250 255

Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys  
 260 265 270

Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly  
 275 280 285

Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn  
 290 295 300

Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe  
 305 310 315 320

Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg  
 325 330 335

Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr  
 340 345 350

Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr  
 355 360 365

Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu

370		375		380
Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr				
385		390		395 400
Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn				
	405		410	415
Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly				
	420		425	430
Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln				
	435		440	445
Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp				
	450		455	460
Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe				
465		470		475 480
Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp				
	485		490	495
Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly				
	500		505	510
Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly				
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Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu				
	530		535	540
Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile				
545		550		555 560
Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg				
	565		570	575
Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr				
	580		585	590
Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser				
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Tyr Leu Lys Gly Ser Arg Ala Lys His Asn				
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 aaaagatcag cagcatctga aagtaaccac tatgcccaacc acatagccaa acagcagtca 600  
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 ggttgaagggt gtacctttat ctacacagtgt gggacctcaa ggctatttct acccaatcca 1020  
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 agaggtatat gaaacagcag aagacaggga caaaaacagc aagcccaatg actggactgt 1140  
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 gttcattgtc ccagaaacca gtgaagggtgt atccttgcaa ctggggaaca caaaagattt 1260  
 tattatttca tttgacctca agttcttaac aaatggaagc gtgtctgtgg ttctggagac 1320  
 gacagaaaag aatcagctct tcaactgtaca ttatgtctca aataccagc taattgcttt 1380  
 taaagaaaga gacataact atggcatcgg gcccagaaca tcatggagca cagttacccg 1440  
 ggacctggtc actgacctca ggaaaggagt gggctcttcc aacacaaaag ctgtcaagcc 1500

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aacaagaata atgccaaga aggtggtag gttgattgcg aaaggaagg gcttccttga 1560
caacattacc atctctacca cagcccatc ggctgccttc ttcgctgcca gtgactggct 1620
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ggcaacagcc ccttacaagt ttctgtcaga gcagcatgga gtcaaggctg tgtttatgaa 1860
taaakatgac tggatgaag aatatccaac tacacctagc tcttttgttt taaatggctt 1920
tatgtattct ttaattgggc tgtatgactt aaaagaaact gcaggggaaa aactcgggaa 1980
agaagcgagg tccttgtagt agcgtggcat ggaatccctt aaagccatgc tccccttgta 2040
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cctggccgcg tgggactatc acaccacca catcaatcaa ctgcagctgc ttagcaccat 2160
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<213> Mus sp.

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Cys Ala Leu Phe Thr Leu Val Thr Val Leu Leu Ser Asp Lys Ala Ile
          20           25           30

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Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg Val Asp Gly Leu Glu
          35           40           45

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Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr Ala Asn His Ile Ala
          50           55           60

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Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu Gln Gln Lys Ala Pro
65           70           75           80

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Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly Ser Lys Tyr Glu Glu
          85           90           95

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Ile Asp Cys Leu Ile Asn Asp Glu His Thr Ile Lys Gly Arg Arg Glu
          100          105          110

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Gly Asn Glu Val Phe Leu Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp  
 115 120 125

Val Tyr Gly Lys Val Val Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe  
 130 135 140

Ser His Ser Tyr Ser Lys Val Tyr Ala Gln Arg Ser Pro Asp Gly Val  
 145 150 155 160

Phe Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys  
 165 170 175

Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro  
 180 185 190

Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His  
 195 200 205

Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Arg  
 210 215 220

Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly Cys Phe  
 225 230 235 240

Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys Gln Phe  
 245 250 255

Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly Asn Thr  
 260 265 270

Lys Asp Phe Ile Ile Ser Phe Asp Asn Gly Ser Val Ser Val Val Leu  
 275 280 285

Glu Thr Thr Glu Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn  
 290 295 300

Thr Gln Leu Ile Ala Phe Arg Asp Arg Asp Ile Tyr Tyr Gly Ile Gly  
 305 310 315 320

Pro Arg Thr Ser Trp Ser Thr Val Thr Asp Leu Arg Lys Gly Val Gly  
 325 330 335

Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys  
 340 345 350

Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr  
 355 360 365

Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp  
 370 375 380

Leu Val Arg Asn Gln Asp Glu Lys Gly Ile Met Val Thr Arg Lys Leu  
 385 390 395 400

Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala  
 405 410 415

Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys  
 420 425 430

Asp Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys  
 435 440 445

Phe Pro Ser Glu Gln His Gly Val Lys Ala Val His Asp Trp Tyr Glu  
 450 455 460

Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly Phe Met Tyr  
 465 470 475 480

Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly Glu Thr Leu  
 485 490 495

Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu Ser Leu Lys  
 500 505 510

Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr His Phe Met Leu  
 515 520 525

Gly Ile Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile  
 530 535 540

Asn Gln Leu Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys  
 545 550 555 560

Glu Phe Val Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys  
 565 570 575

His Asn

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 <211> 434  
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 <213> Bovine lung

<400> 5

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 35 40 45

Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His  
 50 55 60

Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Arg  
 65 70 75 80

Asp Lys Asn Ser Lys Pro Asn Asp Trp Thr Val Pro Lys Gly Cys Phe  
 85 90 95

Met Ala Ser Val Ala Asp Lys Ser Arg Phe Thr Asn Val Lys Gln Phe  
 100 105 110

Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly Asn Thr  
 115 120 125

Lys Asp Phe Ile Ile Ser Phe Asp Asn Gly Ser Val Ser Val Val Leu  
 130 135 140

Glu Thr Thr Glu Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn  
 145 150 155 160

Thr Gln Leu Ile Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly  
 165 170 175

Pro Arg Thr Ser Trp Ser Thr Val Thr Asp Leu Arg Lys Gly Val Gly  
 180 185 190

Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys Lys  
 195 200 205

Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr  
 210 215 220

Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp  
 225 230 235 240

Leu Val Arg Asn Gln Asp Glu Lys Gly Ile Met Val Thr Arg Lys Leu  
 245 250 255

Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala  
 260 265 270

Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys  
 275 280 285

Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys  
 290 295 300

Phe Leu Ser Glu Gln His Gly Val Lys Ala Val His Asp Trp Tyr Glu  
 305 310 315 320

Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly Phe Met Tyr  
 325 330 335

Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly Glu Lys Leu  
 340 345 350

Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu Ser Leu Lys  
 355 360 365

Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr His Phe Met Leu  
 370 375 380

Gly Ile Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile  
 385 390 395 400

Asn Gln Leu Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys  
 405 410 415

Glu Phe Val Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys  
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His Asn

<210> 6  
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 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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 20 25 30

Gly Phe Arg Val Asp Gly Phe Glu Lys Arg Ala Ala Ala Ser Glu Ser  
 35 40 45

Asn Asn Tyr Met Asn His Val Ala Lys Gln Gln Ser Glu Glu Ala Phe  
 50 55 60

Pro Gln Glu Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser  
 65 70 75 80

Asn Val Gly Ser Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn Asp Glu  
 85 90 95

His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu Pro Phe  
 100 105 110

Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val Gln Tyr  
 115 120 125

Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys Val Tyr  
 130 135 140

Ala Gln Arg Ala Pro Asp Gly Val Phe Met Ser Phe Glu Gly Tyr Asn  
 145 150 155 160

Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser Gly Val Glu Gly Val  
 165 170 175

Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln  
 180 185 190

Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys Asn Leu Thr Glu Lys  
 195 200 205

Pro Pro His Ile Glu Val Tyr Arg Asp Lys Asn Lys Pro Asn Asp Trp  
 210 215 220

Thr Val Pro Lys Gly Cys Phe Met Ala Asn Val Ala Asp Lys Ser Arg

225		230		235		240
Phe Thr Asn Val	Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val					
	245		250			255
Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Asn						
	260		265			270
Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe						
	275		280			285
Thr Ile His Tyr Val Ser Asn Ala Gln Leu Ile Ala Phe Lys Glu Arg						
	290		295			300
Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr						
	305		310			315
Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr Lys Ala Val Lys Pro						
	325		330			335
Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu Ile Ala Lys Gly Lys						
	340		345			350
Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr Ala His Met Ala Ala						
	355		360			365
Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn Gln Asp Glu Lys Gly						
	370		375			380
Ile Met Val Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro						
	385		390			395
Gly Trp Tyr Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val						
	405		410			415
Arg Ala Tyr Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu						
	420		425			430
Arg Ala Thr Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys						
	435		440			445
Ala Val His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe						
	450		455			460
Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys						
	465		470			475
						480

Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu  
                     485                    490                    495

Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly  
                     500                    505                    510

Ser Gly Thr His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg Trp  
                     515                    520                    525

Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr Ile  
                     530                    535                    540

Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser Tyr  
                     545                    550                    555                    560

Leu Lys Gly Ser Arg Ala Lys His Asn  
                     565

<210> 7  
 <211> 576  
 <212> PRT  
 <213> Drosophila sp.

<400> 7

Met Ser Lys Tyr Leu Ser Ser Gln Arg Asp Ala Leu Ser Ala Pro Ala  
   1                    5                    10                    15

Leu Pro Val Ser Arg Glu Asn Arg Glu Pro Pro Lys Phe Gln Gly Val  
                     20                    25                    30

Lys Gln Arg Glu Pro Leu Val Phe Phe Ile Met Arg Leu Asn Leu Lys  
                     35                    40                    45

Ala Val Leu Leu Val Leu Thr Val Ala Val Val Val Ile Thr Leu Gly  
                     50                    55                    60

Val Ala Phe Ser Phe Ser Pro Asp Phe Val Arg Pro Leu Asp Arg Ser  
   65                    70                    75                    80

Ala Arg Gln Ser Ser Ser Gly Gly Glu His Asp Ile Glu Cys Ser Ile  
                     85                    90                    95

Asn Gln Glu Tyr Thr Val His Cys Lys Arg Asp Glu Asn Ala Asn Glu  
                     100                    105                    110

Val	Tyr	Val	Pro	Phe	Ser	Phe	Leu	Arg	Asn	Tyr	Phe	Asp	Val	Ser	Gly	115	120	125
Ala	Val	Ser	Thr	Asn	Ser	Asn	Glu	Val	Ala	Lys	Phe	Asn	Trp	Val	His	130	135	140
Ser	Thr	Ala	Lys	Val	Asn	Leu	Pro	Arg	Gly	Lys	Arg	Gly	Val	Tyr	Met	145	150	155
Tyr	Phe	Glu	Asn	Tyr	Asn	Val	Glu	Val	Arg	Asp	Arg	Val	Lys	Cys	Ile	165	170	175
Ser	Ala	Ala	Glu	Gly	Val	Pro	Val	Ser	Thr	Gln	Trp	Glu	Lys	Arg	Gly	180	185	190
Tyr	Phe	Tyr	Pro	Thr	Gln	Ile	Ala	Gln	Phe	Ala	Leu	Ser	His	Tyr	Ser	195	200	205
Lys	Asn	Leu	Thr	Glu	Pro	Ala	Pro	Arg	Val	Arg	Val	Leu	Gly	Asp	Gly	210	215	220
Asn	Gln	Met	Glu	Trp	Ser	Thr	Pro	Lys	Thr	Ser	Asn	Met	Thr	Arg	Ile	225	230	235
Trp	His	His	Lys	Phe	Asn	Thr	Ser	Val	Val	Gln	Phe	Glu	Thr	Ala	Pro	245	250	255
Gly	Tyr	Glu	Gly	Val	Ile	Ser	Ile	Ala	Leu	Asn	Gln	Thr	Leu	Asp	Leu	260	265	270
Leu	Leu	Ser	Val	Asp	Asn	Ser	Ser	Ser	Leu	Met	Ile	Thr	Val	Gln	Asn	275	280	285
Arg	Asp	Thr	Arg	His	Asn	Tyr	Ser	Leu	His	Tyr	Ile	Pro	Ala	Asp	Leu	290	295	300
Leu	Leu	Ser	Val	Gln	Asp	Thr	Asn	Ile	Tyr	Tyr	Gly	Leu	Gly	Gly	Ser	305	310	315
Ala	Leu	Asn	Lys	Trp	Arg	His	Ile	Thr	Asp	Leu	Gln	Lys	Gly	Ile	Met	325	330	335
Gly	Asp	Lys	Arg	Ser	Pro	Leu	Lys	Ile	Arg	Arg	Ser	Asp	Leu	Glu	Val	340	345	350
Ile	Ser	Ile	Gly	Phe	Leu	Gly	Leu	Gly	Phe	Phe	Asp	Asn	Ile	Thr	Leu			



355	360	365
Ser Thr Ser Asp His Leu Ala His Phe Tyr Asp Ala Ala Glu Trp Phe 370 375 380		
Val His Asn Gln Asp Pro Lys Thr Gly Val Arg Arg Ser Leu Asn Gly 385 390 395 400		
Phe Ala Glu Leu Arg Pro Gly Trp Ile Ser Ala Met Gly Gln Gly His 405 410 415		
Ala Ile Ser Val Leu Ala Arg Ala Tyr Trp His Ser Gly Gly Asp Glu 420 425 430		
Arg Tyr Leu Arg Ala Ala Ala Ala Gly Leu Gln Pro Tyr Arg Val Tyr 435 440 445		
Ser Arg Asp Gly Gly Val Leu Ala Gln Phe Tyr Trp Tyr Glu Glu Tyr 450 455 460		
Pro Thr Thr Pro Pro Ser Tyr Val Leu Asn Gly Phe Ile Tyr Ser Leu 465 470 475 480		
Leu Gly Leu Tyr Asp Leu Asn Ser Thr Ala Pro Gly Lys Ile Ala Arg 485 490 495		
Glu Ala Gly Lys Leu Phe Ala Gln Gly Met His Ser Leu Lys Lys Met 500 505 510		
Leu Leu Leu Phe Asp Thr Gly Ser Gly Thr His Leu Ser Leu Gly Val 515 520 525		
Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Ala Thr His Val Asn Gln 530 535 540		
Leu Leu Leu Leu Ala Thr Ile Asp Ser Asp Pro Leu Ile Ala Gln Thr 545 550 555 560		
Ala Glu Arg Trp Lys Gly Tyr Met Phe Gly Arg Arg Ala Lys His Asn 565 570 575		

<210> 8  
 <211> 599  
 <212> PRT  
 <213> C. elegans  
 <400> 8

Met Val Leu Val Ser Leu Lys Pro Phe Asn Ile Phe Ser Leu Lys Pro  
 1 5 10 15  
 Met Lys Cys Leu Arg Trp Arg Ser Asn Arg His Arg Ile Tyr Leu Leu  
 20 25 30  
 Val Ala Cys Gly Ala Leu Phe Leu Leu Arg His Leu Thr Gln Glu Glu  
 35 40 45  
 Ser Arg Ile Asp Glu Glu Asp Glu Glu Leu Thr Gln Val Asp Val Asn  
 50 55 60  
 Glu Asp Asp Lys Lys Ile Glu Cys Glu Pro Pro Gly Ser Ile Glu Ser  
 65 70 75 80  
 Lys Cys Ile Ala Asp Asn Gly Lys Ser Met Lys Cys Trp Lys Asp Glu  
 85 90 95  
 Glu Asp Val Tyr Phe Pro Val Ser Tyr Leu Lys Lys Arg Phe Asp Met  
 100 105 110  
 Thr Gly Lys Leu Gly Lys Asp Gly Ser Thr Phe Glu Leu Tyr Thr Ser  
 115 120 125  
 Tyr Ala Lys Met Arg Ser Pro Asp Leu Gly Pro Phe Gly His Phe Ser  
 130 135 140  
 Thr Tyr Ser Val Glu Thr Arg Asp Arg Val Arg Cys Val Ser Ala Lys  
 145 150 155 160  
 Thr Asp Val Pro Met Ser Thr Gln Trp Asp Pro Ile Pro Tyr Tyr Tyr  
 165 170 175  
 Pro Ile Gln Ile Ser Gln Tyr Gly Leu Gln His Tyr Ser Arg Met Lys  
 180 185 190  
 Leu Asp Ser Ile Ser Asn Lys Ser Glu Ala Ser Pro Lys Asp Asp Val  
 195 200 205  
 Ile Asn Ser Lys Glu Trp Lys Gly Ala Ala Gly Met His Glu Thr Thr  
 210 215 220  
 Glu Arg Leu Phe Phe Asn Asp Glu Gln Met Gly Lys Val Val Asn Ile  
 225 230 235 240

Ser Ala Gly Ala Ala Leu Ala Asn Ala Gly Ala Tyr Val Tyr Leu Asp  
 245 250 255

Lys Ser Pro Asp Leu His Val Ile Ser Phe Asp Ala Asn Ser Ser Phe  
 260 265 270

Thr Val Leu Ala Lys Met Lys Gln Asp Asp Leu Leu Val Leu Ile Asn  
 275 280 285

Tyr Val Tyr Ser Glu Gly Asn Gly Lys Cys Val Trp Gln Glu Glu Glu  
 290 295 300

Arg Ile Ser Asp Asp Tyr Ile Val Gln Lys Pro Lys Lys Asp Gly Gln  
 305 310 315 320

Val Ser Tyr Ser Tyr Ser Tyr Ile Gly Asn Ser Pro Ile Gly Glu Trp  
 325 330 335

Ser Thr Val Thr Asp Val Ala Arg Ala Leu Ser Ser Gly Asp Asn Arg  
 340 345 350

Lys Lys Asp Asp Asn Val Val Leu His Ala Gly Asp Leu Arg Leu Val  
 355 360 365

Ser Leu Gly Phe Arg Gly Glu Leu Thr Val Lys Gln Lys Ile Thr Gln  
 370 375 380

Arg Arg Glu Gln His Ser His Ala Phe Tyr Ala Ala Ala Asp Trp Leu  
 385 390 395 400

Val Lys Asn Gln Asn Asp Arg Gly Val Glu Arg Ser Ile Ala Glu Arg  
 405 410 415

Lys Leu Val Leu Pro Pro Gly Trp His Ser Ala Met Ala Gln Gly His  
 420 425 430

Gly Ile Ser Val Leu Thr Arg Ala Phe Lys His Phe Asn Asp Glu Lys  
 435 440 445

Tyr Leu Lys Ser Ala Ala Lys Ala Leu Lys Leu Phe Lys Ile Asn Ser  
 450 455 460

Ser Asp Gly Gly Val Arg Gly Glu Ile Trp Tyr Glu Glu Tyr Pro Thr  
 465 470 475 480

Thr Pro Gly Ser Phe Val Leu Asn Gly Phe Leu Tyr Ser Leu Ile Gly

485

490

495

Leu Tyr Asp Leu Ser Gln Leu Glu Leu Met Ile Asp Glu Asn Asp Glu  
 500 505 510

Thr Met Arg Ala Lys Ile Gln Glu Ala Gln Glu Leu Tyr Ser Ala Gly  
 515 520 525

Val Arg Ser Leu Lys Gln Leu Leu Pro Leu Tyr Asp Thr Gly Ser Gly  
 530 535 540

Thr His Val Ala Leu Gly Thr Ala Pro Asn Leu Ala Arg Trp Asp Tyr  
 545 550 555 560

His Ala Val His Val Tyr Leu Leu Lys Trp Ile Ala Gly Ile Glu Lys  
 565 570 575

Asp Glu Val Leu Ser Lys Thr Ala Asp Arg Trp Ile Gly Tyr Ala Tyr  
 580 585 590

Gly Lys Arg Ala Lys His Asn  
 595

<210> 9  
 <211> 216  
 <212> PRT  
 <213> Methanococcus sp.

<400> 9

Met Ile Leu Met Lys Lys Phe Glu Ile Ile Leu Phe Leu Phe Ile Ala  
 1 5 10 15

Val Leu Ile Phe Val Phe Gly Phe Val Gly Ala Ser Gln Pro Leu Tyr  
 20 25 30

Ser Glu Asn Pro Val Ile Gln Tyr Phe Lys Asn Pro Lys Pro Phe Thr  
 35 40 45

Val Glu Asn Val Asn Met Pro Val Thr Tyr Tyr Gly Thr Ile Cys Gly  
 50 55 60

Lys Tyr Ile Gly Tyr Gln Ile Thr Pro His Asn Val Asn Glu Glu Ala  
 65 70 75 80

Arg Lys Cys Phe Tyr Lys Tyr Phe Lys Leu Lys Asp Lys Asn Pro Lys  
 85 90 95

Glu Ala Glu Arg Tyr Leu Lys Arg Gly Leu Phe Leu Thr Glu Tyr Leu  
                   100                  105                  110

Ile Ser Gln Ala Asp Lys Glu Thr Ala Glu Val Asp Glu Lys Asn Ile  
           115                  120                  125

Thr Phe Ile Val Trp Arg Tyr Asn Phe Glu Phe Pro Asn Leu Ser Lys  
       130                  135                  140

Gly Trp Arg Gly Ala Leu Cys Gln Ala Gly Cys Leu Lys Thr Leu Tyr  
   145                  150                  155                  160

Leu Ala Tyr Glu Ala Thr Gly Asp Glu Arg Tyr Leu Asn Tyr Ala Asn  
                   165                  170                  175

Leu Ala Ile Asn Ala Phe Lys Val Pro Val Glu Lys Gly Gly Leu Leu  
           180                  185                  190

Lys Ile Arg Ile Tyr Tyr Trp Phe Pro Glu Tyr Ala Ser Glu Asn Pro  
           195                  200                  205

Pro Tyr Val Leu Asn Gly Phe Ile  
       210                  215

<210> 10  
 <211> 174  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Tag that preceded each recombinant construct

<220>  
 <221> CDS  
 <222> (1)..(174)

<400> 10  
 atg act att ctc tgc tgg ctt gcg ctg ttg tca aca ctt acc gcc gtg 48  
 Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser Thr Leu Thr Ala Val  
 1                  5                  10                  15  
  
 aac gca gac tac aag gac gac gat gac aag cgg ccg cat gcg gaa ttc 96  
 Asn Ala Asp Tyr Lys Asp Asp Asp Asp Lys Arg Pro His Ala Glu Phe  
           20                  25                  30  
  
 atg cgg ggt tct cat cac cat cac cat cac gat tac gat atc cca acg 144  
 Met Arg Gly Ser His His His His His His Asp Tyr Asp Ile Pro Thr  
       35                  40                  45  
  
 acc gaa aac ctg tat ttt cag ggc gcc atg 174  
 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met

50

55

&lt;210&gt; 11

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Tag that preceded each recombinant construct

&lt;400&gt; 11

Met	Thr	Ile	Leu	Cys	Trp	Leu	Ala	Leu	Leu	Ser	Thr	Leu	Thr	Ala	Val
1				5					10					15	

Asn	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Arg	Pro	His	Ala	Glu	Phe
			20					25					30		

Met	Arg	Gly	Ser	His	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr
			35					40				45			

Thr	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ala	Met
50						55			